

ABN80300 standard; DNA; 18679 BP.

ABN80300;

15-JUL-2002 (first entry)

Human chemically modified disease associated gene SEQ ID NO 317.

Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.

Homo sapiens.

Synthetic.

WO200200927-A2.

03-JAN-2002.

02-JUL-2001; 2001WO-EP007536.

30-JUN-2000; 2000DE-01032529.

01-SEP-2000; 2000DE-01043826.

(SPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2002-130908/17.

Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development.

Claim 1; SEQ ID NO 317; 27pp; English.

The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or APD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Curriarino syndrome, diseases related to the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

Sequence 18679 BP; 4158 A; 716 C; 5033 G; 8772 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 18679;

Best Local Similarity 100.0%; Pred. No. 6.6;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGAAATCCCAACCAACCAACC 24

11952 CAAGAAATCCCAACCAACCAACC 11929

Db

RESULT 4

ABQ51324/c

ID ABQ51324 standard; DNA; 588 BP.

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